

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=9; day=22; hr=8; min=8; sec=20; ms=559;]

=====

Application No: 10825898

Version No: 2.0

Input Set:

Output Set:

Started: 2009-09-03 20:36:05.926

Finished: 2009-09-03 20:36:08.741

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 815 ms

Total Warnings: 48

Total Errors: 0

No. of SeqIDs Defined: 54

Actual SeqID Count: 54

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)

Input Set:

Output Set:

Started: 2009-09-03 20:36:05.926
Finished: 2009-09-03 20:36:08.741
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 815 ms
Total Warnings: 48
Total Errors: 0
No. of SeqIDs Defined: 54
Actual SeqID Count: 54

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> BOYLE, William J.

<120> OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS

<130> A-451N (A-451BUSRevSeq051408fromA-451K-54Seqs41&44-53)

<140> 10825898

<141> 2004-04-15

<150> US 09/052,521

<151> 1998-03-30

<150> US 08/880,855

<151> 1997-06-23

<150> US 08/842,842

<151> 1997-04-16

<160> 54

<170> PatentIn version 3.3

<210> 1

<211> 2295

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (158)..(1105)

<400> 1

gagctcggat ccactactcg acccacgcgt ccggccagga cctctgtgaa ccggtcgggg 60

cgggggccgc ctggccggga gtctgctcgg cggtgggtgg ccgaggaagg gagagaacga 120

tcgctggagca gggcgcccga actccgggcg ccgcgcc atg cgc cgg gcc agc cga 175
Met Arg Arg Ala Ser Arg
1 5

gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc agc ggc ccc 223
Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
10 15 20

ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct gca ccg gct 271
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
25 30 35

ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg gcc ctc ctg 319
Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
40 45 50

ggg ctg gga ctg ggc cag gtg gtc tgc agc atc gct ctg ttc ctg tac 367

Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Ile	Ala	Leu	Phe	Leu	Tyr	
55					60					65					70	
ttt	cga	gcg	cag	atg	gat	cct	aac	aga	ata	tca	gaa	gac	agc	act	cac	415
Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	Glu	Asp	Ser	Thr	His	
			75					80					85			
tgc	ttt	tat	aga	atc	ctg	aga	ctc	cat	gaa	aac	gca	ggt	ttg	cag	gac	463
Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	Ala	Gly	Leu	Gln	Asp	
			90					95					100			
tcg	act	ctg	gag	agt	gaa	gac	aca	cta	cct	gac	tcc	tgc	agg	agg	atg	511
Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro	Asp	Ser	Cys	Arg	Arg	Met	
		105					110				115					
aaa	caa	gcc	ttt	cag	ggg	gcc	gtg	cag	aag	gaa	ctg	caa	cac	att	gtg	559
Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	Glu	Leu	Gln	His	Ile	Val	
	120					125					130					
ggg	cca	cag	cgc	ttc	tca	gga	gct	cca	gct	atg	atg	gaa	ggc	tca	tgg	607
Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	Met	Met	Glu	Gly	Ser	Trp	
135					140					145				150		
ttg	gat	gtg	gcc	cag	cga	ggc	aag	cct	gag	gcc	cag	cca	ttt	gca	cac	655
Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	Ala	Gln	Pro	Phe	Ala	His	
			155					160				165				
ctc	acc	atc	aat	gct	gcc	agc	atc	cca	tcg	ggc	tcc	cat	aaa	gtc	act	703
Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Thr	
			170					175				180				
ctg	tcc	tct	tgg	tac	cac	gat	cga	ggc	tgg	gcc	aag	atc	tct	aac	atg	751
Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	Met	
	185					190					195					
acg	tta	agc	aac	gga	aaa	cta	agg	gtt	aac	caa	gat	ggc	ttc	tat	tac	799
Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	
	200					205					210					
ctg	tac	gcc	aac	att	tgc	ttt	cgg	cat	cat	gaa	aca	tcg	gga	agc	gta	847
Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	Glu	Thr	Ser	Gly	Ser	Val	
215					220					225			230			
cct	aca	gac	tat	ctt	cag	ctg	atg	gtg	tat	gtc	gtt	aaa	acc	agc	atc	895
Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr	Val	Val	Lys	Thr	Ser	Ile	
			235					240				245				
aaa	atc	cca	agt	tct	cat	aac	ctg	atg	aaa	gga	ggg	agc	acg	aaa	aac	943
Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	Asn	
		250						255				260				
tgg	tcg	ggc	aat	tct	gaa	ttc	cac	ttt	tat	tcc	ata	aat	gtt	ggg	gga	991
Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	Gly	
	265					270					275					
ttt	ttc	aag	ctc	cga	gct	ggc	gaa	gaa	att	agc	att	cag	gtg	tcc	aac	1039
Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	Ile	Ser	Ile	Gln	Val	Ser	Asn	

280	285	290	
cct tcc ctg ctg gat ccg gat caa gat gcg acg tac ttt ggg gct ttc			1087
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe			
295	300	305	310
aaa gtt cag gac ata gac tgagactcat ttcgtggaac attagcatgg			1135
Lys Val Gln Asp Ile Asp			
315			
atgtcctaga tgtttggaac cttcttaaaa aatggatgat gtctatacat gtgtaagact			1195
actaagagac atggcccacg gtgtatgaaa ctcacagccc tctctcttga gcctgtacag			1255
gttgtgtata tgtaaagtcc ataggtgatg ttagattcat ggtgattaca caacggtttt			1315
acaattttgt aatgatttcc tagaattgaa ccagattggg agaggtattc cgatgcttat			1375
gaaaaactta cacgtgagct atggaagggg gtcacagtct ctgggtctaa cccctggaca			1435
tgtgccactg agaaccttga aattaagagg atgccatgtc attgcaaaga aatgatagtg			1495
tgaagggtta agttcttttg aattgttaca ttgcgctggg acctgcaaata aagttctttt			1555
tttctaataga ggagagaaaa atatatgtat ttttatataa tgtctaaaagt tatatttcag			1615
gtgtaatgtt ttctgtgcaa agttttgtaa attatatattg tgctatagta tttgattcaa			1675
aatatttaaa aatgtctcac tgttgacata ttaaatgttt taaatgtaca gatgtattta			1735
actgggtgcac tttgtaattc ccctgaaggt actcgtagct aagggggcag aatactgttt			1795
ctgggtgacca catgtagttt atttctttat tctttttaac ttaatagagt cttcagactt			1855
gtcaaaacta tgcaagcaaa ataaataaat aaaaataaaa tgaatacctt gaataataag			1915
taggatgttg gtcaccaggt gcctttcaaa tttagaagct aattgacttt aggagctgac			1975
atagccaaaa aggatacata ataggctact gaaatctgtc aggagtattt atgcaattat			2035
tgaacaggtg tcttttttta caagagctac aaattgtaaa ttttgtttct tttttttccc			2095
atagaaaatg tactatagtt tatcagccaa aaaacaatcc actttttaat ttagtgaaag			2155
ttattttatt atactgtaca ataaaagcat tgtctctgaa tgtaattttt ttggtacaaa			2215
aaataaattt gtacgaaaac ctgaaaaaaa aaaaaaaaaa aaaaaaaagg gcggccgctc			2275
tagaggggccc tattctatag			2295

<210> 2
 <211> 316
 <212> PRT
 <213> Mus musculus

<400> 2

Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Gly	Lys	Tyr	Leu	Arg	Ser	Ser	Glu	1	5	10	15
Glu	Met	Gly	Ser	Gly	Pro	Gly	Val	Pro	His	Glu	Gly	Pro	Leu	His	Pro	20	25	30	
Ala	Pro	Ser	Ala	Pro	Ala	Pro	Ala	Pro	Pro	Pro	Ala	Ala	Ser	Arg	Ser	35	40	45	
Met	Phe	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	50	55	60	
Ile	Ala	Leu	Phe	Leu	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	65	70	75	80
Ser	Glu	Asp	Ser	Thr	His	Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	85	90	95	
Asn	Ala	Gly	Leu	Gln	Asp	Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro	100	105	110	
Asp	Ser	Cys	Arg	Arg	Met	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	115	120	125	
Glu	Leu	Gln	His	Ile	Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	130	135	140	
Met	Met	Glu	Gly	Ser	Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	145	150	155	160
Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser	165	170	175	
Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	180	185	190	
Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	195	200	205	
Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	210	215	220	

```

<400>      3
aagcttggtgta ccgagctcgg atccactact cgacccacgc gtcgcgcgcgc cccaggagacc      60

aaagccggggc tccaagtcgg cgccccacgt cgaggctccg ccgcagcctc cggagttggc      120

cgcagacaag aagggggaggg agcggggagag ggaggagagc tccgaagcga gaggggccgag      180

cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg      229
Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
      1          5          10          15

gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac      277
Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
      20          25          30

gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc      325
Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
      35          40          45

atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc      373
Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
      50          55          60

```

gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata	421
Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
65 70 75	
tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa	469
Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu	
80 85 90 95	
aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta	517
Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu	
100 105 110	
ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg	565
Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val	
115 120 125	
caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag	613
Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu	
130 135 140	
aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag	661
Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys	
145 150 155	
ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc	709
Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile	
160 165 170 175	
cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg	757
Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg	
180 185 190	
ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata	805
Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile	
195 200 205	
gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga	853
Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg	
210 215 220	
cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg	901
His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met	
225 230 235	
gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg	949
Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu	
240 245 250 255	
atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat	997
Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His	
260 265 270	
ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag	1045
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu	
275 280 285	
gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag	1093

Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
 290 295 300

gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat 1135
 Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 305 310 315

tgagccccag tttttggagt gttatgtatt tcttgatgt ttggaacat tttttaaaac 1195
 aagccaagaa agatgtatat aggtgtgtga gactactaag aggcattggc ccaacggtac 1255
 acgactcagt atccatgctc ttgacctgt agagaacacg cgtatttaca gccagtggga 1315
 gatgttagac tcatgggtgtg ttacacaatg gtttttaaata tttgtaata attcctagaa 1375
 ttaaaccaga ttggagcaat tacgggttga ccttatgaga aactgcatgt gggctatggg 1435
 aggggttggc cctgggtcat gtgccccttc gcagctgaag tggagagggt gtcattctagc 1495
 gcaattgaag gatcatctga aggggcaaata tcttttgaat tgttacatca tgctggaacc 1555
 tgcaaaaaat actttttcta atgaggagag aaaatatatg tttttttata taatatctaa 1615
 agttatatat cagatgtaat gttttctttg caaagtattg taaattatat ttgtgctata 1675
 gtatttgatt caaaatatat aaaaatgtct tgctgttgac atatttaata ttttaaatgt 1735
 acagacatat ttaactggtg cactttgtaa attccctggg gaaaacttgc agctaaggag 1795
 gggaaaaaaa tgttggttcc taatatcaaa tgcagtatat ttcttcgttc tttttaagtt 1855
 aatagatttt ttcagacttg tcaagcctgt gcaaaaaaat taaaatggat gccttgaata 1915
 ataagcagga tgttggtccac cagggtgcctt tcaaatttag aaactaattg acttttagaaa 1975
 gctgacattg ccaaaaagga tacataatgg gccactgaaa tctgtcaaga gtagttatat 2035
 aattgttgaa cagggtgtttt tccacaagtg ccgcaaattg tacctttttt tttttttcaa 2095
 aatagaaaag ttattagtgg tttatcagca aaaaagtcca attttaattt agtaaatgtt 2155
 atcttatact gtacaataaa aacattgcct ttgaatgtta attttttggg acaaaaataa 2215
 atttatatga aaaaaaaaaa aaaagggcgg ccgctctaga gggccctatt ctatag 2271

<210> 4
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
 1 5 10 15

Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala		
20	25	30
Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met		
35	40	45
Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val		
50	55	60
Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser		
65	70	75
Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn		
85	90	95
Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile		
100	105	110
Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln		
115	120	125
Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys		
130	135	140
Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu		
145	150	155
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro		
165	170	175
Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly		
180	185	190
Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val		
195	200	205
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe		